JOURNAL OF BACTERIOLOGY, Sept. 1990, p. 4746–4747
0021-9193/90/094746-02$02.00/0

Vol. 172, No. 9

Locations of Genes in the 52-Minute Region on the Physical Map of *Escherichia coli* K-12

YVES V. BRUN† AND JACQUES LAPOINTE*

Département de Biochimie, Faculté des Sciences et de Génie, Université Laval, Ste-Foy, Québec, Canada G1K 7P4

To order and orient the markers in the 52-min region of the *Escherichia coli* K-12 chromosome for our evolutionary studies of this region, we compared the restriction map information available for genes mapped in this region with that of the physical map of Kohara et al. (10). Taking into account the position of the *crr* gene indicated by Kohara et al. (10), we scanned 1 min on each side of *crr* for the best correspondence to the published physical maps of the cloned genes from this region.

There is a very good correspondence between the two maps, but there are some small discrepancies. These are discussed by Brun et al. (Y. V. Brun, R. Breton, P. Lanovette, and J. Lapointe, J. Mol. Biol., in press) and are mostly due to imprecisions caused by the methods used for the construction of the physical map (see results in reference 10) or by polymorphism between strains (1, 7).

A report of the cloning of *glk* has been published (6), but since *glk* was cloned from *E. coli* B, it is hard to correlate its restriction map with that of the *E. coli* K-12 chromosome physical map. Indeed, Anilionis and Riley (1) have shown that different strains of *E. coli* can show a substantial degree of nucleotide sequence variation (5 to 25%). The best correspondence that can be found in the 20-kilobase-pair (kb) region on the counterclockwise side of the *Eco*RV fragment downstream from *gltX* is with the 13-kb *Hin*dIII fragment starting just clockwise from position 2520 kb and going toward the left of the map. Three of the four *Pst*I sites, two of the four *Eco*RI sites, and one of the *Hin*dIII sites can be correlated approximately, but the correspondence is far from convincing. Nevertheless, it is probable that *glk* lies within 10 kb of *gltX* at the most (Brun et al., in press).

We were, however, able to position most of the cloned markers of the 52-min region, all of which are physically linked by common restriction sites, on the physical map (Table 1). This knowledge was subsequently used to deduce the positions of the other markers. Thus, the order of the 18 genes in this region is *nupC-glk-*<(*alaW*β-*alaW*α)-1 kb-<*gltX*-0.3 kb-(*valU*α-*valU*β-*valU*γ-*lysV*=*supN*)>-*xapR-xapA-*<*lig*-1 kb-*cysK*>-0.4 kb-*ptsH*>-0.05 kb-*ptsI*>-0.05 kb-*crr*>-*cysM-cysA*, in clockwise order (> and < indicate the direction of transcription) (Brun et al., in press).

TABLE 1. Physical locations of genes in the 52-min region of the *E. coli* K-12 chromosome

Gene	Genetic map location (min)[a]	Physical map location[b]		Strain[c] (reference)	Additional comments
		min	kb		
nupC	51.79	(53.3)		(2)	Nucleoside transport system
glk	51.90	(53.3)		*E. coli* B (6)	Glucokinase
*alaW*αβ	—[d]	53.62	2531	N99 (Brun et al., in press)	Two identical $tRNA^{Ala}_{GGC}$
gltX	52.05	53.67	2533	N99 (3)	Glutamyl-tRNA synthetase
*valU*αβγ	—[d]	53.69	2534	N99 (Brun et al., in press)	Three identical $tRNA^{Val}_{UAC}$
lysV	52.00	53.69	2534	AB2547 (13)	Wild-type allele of *supN*
				N99 (Brun et al., in press)	$tRNA^{Lys}_{UUU}$ in *valU* operon
xapR	51.90	[53.7]	[2535]	(4, 9)	Regulatory gene for *xapAR*
xapA	51.90	[53.8]	[2537]	(4)	Xanthosine phosphorylase
lig	52.10	53.81	2540	C600 (8)	DNA ligase
cysK	52.31	53.91	2545	N99 (5)	Cysteine synthase
ptsH	52.21	53.94	2546	N99 (5)	Phosphohistidinoprotein-
				DG2 (11)	hexose phosphotransferase HPr
ptsI	52.21	53.96	2547	N99 (5)	Phosphotransferase system
				DG2 (11)	Enzyme I
crr	52.26	53.98	2548	N99 (5), DG2 (11)	Enzyme III^{Glc}
cysM	—[d]	54.04	2551	XPh43 (12)	*o*-Acetylserine sulfydrylase B
cysA	52.31	54.04	2551	XPh43 (12)	Sulfate permease

[a] From reference 2.
[b] Positions in minutes are derived from the exact physical position in kilobase pairs by multiplying by 47.2. Brackets indicate positions deduced for genes strongly suspected to lie close to physically mapped genes (Brun et al., in press). Parentheses indicate positions deduced from comparison of the physical and linkage maps (Brun et al., in press).
[c] Strain from which the DNA used for the restriction mapping was cloned.
[d] Not on the linkage map in reference 2.

* Corresponding author.
† Present address: Department of Developmental Biology, Beckman Center, Stanford University Medical Center, Stanford, CA 94305-5427.

ADDENDUM IN PROOF

The order of genes agrees with that published in edition 8 of the *E. coli* linkage map (2a).

LITERATURE CITED

1. **Anilionis, A., and M. Riley.** 1980. Conservation and variation of nucleotide sequences within related bacterial genomes: *Escherichia coli* strains. J. Bacteriol. **143:**355–365.
2. **Bachmann, B. J.** 1987. Linkage map of *Escherichia coli* K-12, edition 7, p. 807–876. *In* F. C. Neidhardt, K. B. Low, J. L. Ingraham, B. Magasanik, M. Schaechter, and H. E. Umbarger (ed.), *Escherichia coli* and *Salmonella typhimurium*: cellular and molecular biology. American Society for Microbiology, Washington, D.C.

2a. **Bachmann, B. J.** 1990. Linkage map of *Escherichia coli* K-12, edition 8. Microbiol. Rev. **54:**130–197.

3. **Breton, R., H. Sanfaçon, I. Papayannopoulos, K. Biemann, and J. Lapointe.** 1986. Glutamyl-tRNA synthetase of *Escherichia coli*. Isolation and primary structure of the *gltX* gene and homology with other aminoacyl-tRNA synthetases. J. Biol. Chem. **261:**10610–10617.
4. **Buxton, R. S., K. Hammer-Jespersen, and P. Valentin-Hansen.** 1980. A second purine phosphorylase in *Escherichia coli* K-12. I. Xanthosine phosphorylase regulatory mutants isolated as secondary-site revertants of a *deoD* mutant. Mol. Gen. Genet. **179:**331–340.
5. **De Reuse, H., and A. Danchin.** 1988. The *ptsH*, *ptsI*, and *crr* genes of the *Escherichia coli* phosphoenolpyruvate-dependent phosphotransferase system: a complex operon with several modes of transcription. J. Bacteriol. **170:**3827–3837.
6. **Fukuda, Y., S. Yamaguchi, M. Shimosaka, K. Murata, and A. Kimura.** 1983. Cloning the glucokinase gene in *Escherichia coli* B. J. Bacteriol. **156:**922–925.
7. **Harshman, L., and M. Riley.** 1980. Conservation and variation of nucleotide sequences in *Escherichia coli* strains isolated from nature. J. Bacteriol. **144:**560–568.
8. **Ishino, Y., H. Shinagawa, K. Makino, S. Tsunasawa, F. Sakiyama, and A. Nakata.** 1986. Nucleotide sequence of the *lig* gene and primary structure of DNA ligase of *Escherichia coli*. Mol. Gen. Genet. **204:**1–7.
9. **Kocharyan, S. M., and M. A. Melkumyan.** 1986. Genetic study of *Escherichia coli* K-12 mutants defective for structural and regulatory genes of second purine nucleoside phosphorylase. Genetika **22:**2055–2065.
10. **Kohara, Y., K. Akiyama, and K. Isono.** 1987. The physical map of the whole *E. coli* chromosome: application of a new strategy for rapid analysis and sorting of a large genomic library. Cell **50:**495–508.
11. **Saffen, D. W., K. A. Presper, T. L. Doering, and S. Roseman.** 1987. Sugar transport by the bacterial phosphotransferase system. Molecular cloning and structural analysis of the *Escherichia coli ptsH*, *ptsI*, and *crr* genes. J. Biol. Chem. **262:** 16241–16253.
12. **Sirko, A. E., M. Zatyka, and M. D. Hulanicka.** 1987. Identification of the *Escherichia coli cysM* gene encoding o-acetylserine sulphydrylase B by cloning with mini-mu-*lac* containing a plasmid replicon. J. Gen. Microbiol. **133:**2719–2725.
13. **Uemura, H., S. Thorbjarnardottir, V. Gamulin, J. Yano, O. S. Andresson, D. Soll, and G. Eggertsson.** 1985. *supN* ochre suppressor gene in *Escherichia coli* codes for $tRNA^{Lys}$. J. Bacteriol. **163:**1288–1289.